

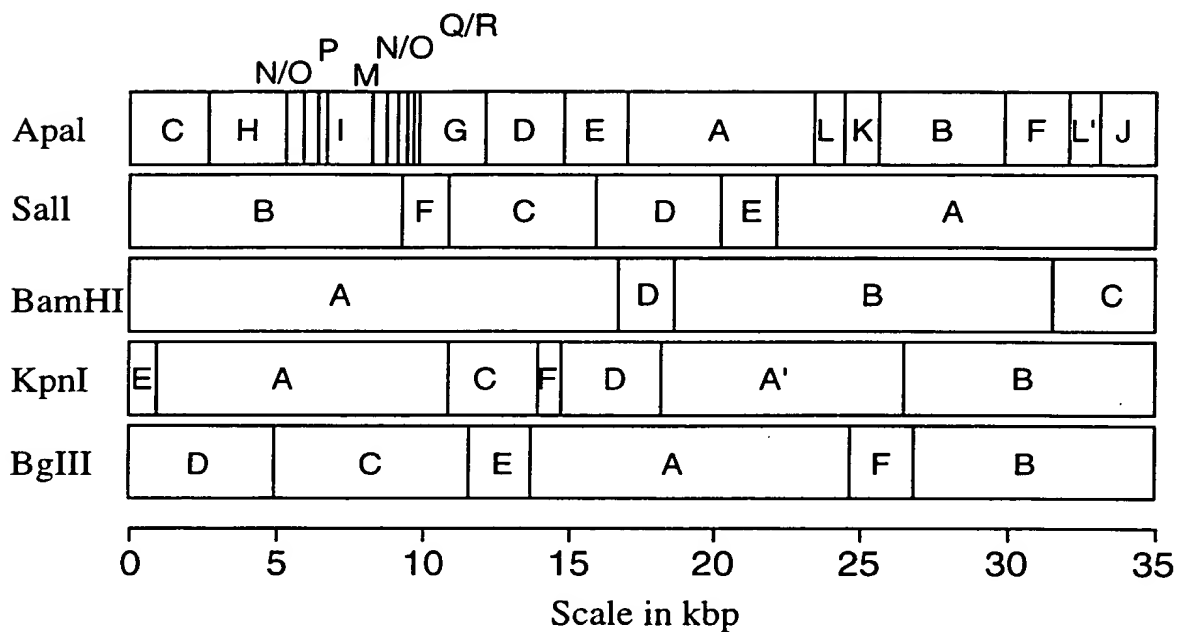
APPROVED	C.E. FIG.	
BY	CLASS	SUBCLASS
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ART 34  
PCT/AU98/00648  
Received 11 November 1999  
09/485512

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Fig 1.

Restriction enzyme maps of the PAV3 genome



APPROVED	O.G. FIG.	
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Fig 2.

Total sequence of the PAV Major Late Promoter cassette including the added nucleotides 5' (upstream) of the USF.

Nucleotide base count: 76 A 143 C 187 G 96 T Total 502 bp

```

1  GGTGCCGCGG TCGTCGGCGT AGAGGATGAG GGCCCGAGTCG GAGATGAAGG CACGCGCCCA
61  GCGGAGGACG AAGCTGGCGA CCTGCGAGGG GTAGCGGTCG TTGGGCACTA ATGGCGAGGC
121 CTGCTCGAGC GTGTGGAGAC AGAGTCCTC GTCGTCCGCG TCCAGGAAGT GGATTGGTCG
181 CCAGTGGTAG TCCACGTGAC CGGCTTCCGG GTCGGGGGGT ATAAAGGCGCGGCCGGGG
241 TCGGTGGCCG TCAGTTGCTT CGCAGGCCTC GTCACCGGAG TCCGCGTCTC CGGCGTCTCG
301 CGCTGCGGCT GCATCTGTGG TCCCGGAGTC TTCAGGTCCT TGTGAGGAG GTACTCCTGA
361 TCGCTGTCCC AGTACTTGGC GTGTGGGAAG CCGTCCTGAT CGCGATCCTC CTGCTGTTGC
421 AGCGCTTCGG CAAACACGCG CACCTGCTCT TCGGACCCGG CGAAGCGTTC GACGAAGGCG
481 TCTAGCCAGC AACAGTCGCA AG
  
```

The Upstream Stimulatory Factor (USF) and TATA motif are in **bold**. The complete leader sequence is italicised with the cap site and splice sites between the individual leaders indicated by double underlining or single underlining respectively.

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## Fig 3.

Individual sequences of the Promoter cassette components:

### I. The 5' (upstream) sequence included in the long cassette.

```

1      GGTGCCGCGG TCGTCGGCGT AGAGGATGAG GGCCAGTCG GAGATGAAGG CACGCGCCCA
61     GGCGAGGACG AAGCTGGCGA CCTGCGAGGG GTAGCGGTCG TTGGGCACTA ATGGCGAGGC
121    CTGCTCGAGC GTGTGGAGAC AGAGGTCCTC GTCGTCCGCG TCCAGGAAGT GGATTGGTCG
181    CCAGTGGTAG

```

### II. Sequence including the USF, TATA motif and sequence to the cap site.

```

1      CCACGTGACC GGCTTGC GGG TCGGGGGGTA TAAAGGCGC GGGCCGGGGT GCGTGGCCGT
61     C

```

### III. First leader sequence.

```

1      AGTTGCTTCG CAGGCCTCGT CACCGGAGTC CGCGTCTCCG GCGTCTCGCG CTGCGGCTGC
61     ATCTGTGGTC CCGGAGTCTT CAG

```

### IV. Second leader sequence.

```

1      GTCCTTGTTG AGGAGGTACT CCTGATCGCT GTCCAGTAC TTGGCGTGTG GGAAGCCGTC
61     CTGATCG

```

### V. Third leader sequence.

```

1      CGATCCTCCT GCTGTTGCAG CGCTTCGGCA AACACGCGCA CCTGCTCTTC GGACCCGGCG
61     AAGCGTTTCA CGAAGGCGTC TAGCCAGCAA CAGTCGCAAG

```

Sequence of the right hand end of the PAV genome this area being a proposed site for insertion of expression cassettes.

Nucleotide base count 183 A 255 C 306 G 204 T Total 948 bases

1 CATCATCAAT AATATACCGC ACACCTTTTAT TGCCCCCTTTT GTGGCGTGTT GATTGGCGGA  
61 GAGGGTTGGG GSCGGCGGGC GGTGATTGGT GGAGAGGGGT GTGACGTAGC GTGGGAACGT  
121 GACGTCGCGT GGGAAAATAA CGTGCGGTGG GAACGGTCAA AGTCCGAGGG GCGGGGTCAA  
181 AGTCCGCAGT CGCGGGGCGG AGCCGGCTGG CGGGAATTCC EcoRI SmaI TGGGCGGGTA  
241 ATCGTTAAGC CGGAGGCGGG GGAATTCGA TCGGACGATG TGGTACTGAT TAACCGACCG  
301 CAGCGGTGTC CACATCCGCT GTGGGTATAT CACCGGCGCT CGCGGTGTTC GCTCACACTC  
361 GTCTCGGCGC TGTCACAGAG AGAGACACTG AGAGCGAGAC GAGGAGAAAC CGAAAGCGGG  
421 GCAGGAGGAG TCACCGGGCC ATCTTCCCAT CAGAGCCCTC TCATGGCCCA CGACCGACTG  
481 CTGCTGGCCG CGGTGGCTGA CTGTTGCTCG CCGTGTCTTA TCTGTACTTC GCCTACCTCG  
541 CGTGGCAGGA TCGGGACACT CTTCACACTC AGGAGGCCGC CTCTCCTCGC TTCTTCATCG  
601 GGTCCAACCA CCAGCCCTGG TGCCCGGATT TTGATTGGCA GGAGCAGGAC GAGCACACTC  
661 ACTAGACGTT TAGAAAAAG ACACACATTG GAACTCATAT ATGTCTGCGG GACCGCATCA  
721 GCAGCCCGGT CTGCTGTTGG CTGCGGGTGA GAGGCTCCG GTAATTCAAT AGAACCAGAT  
781 TCATCTGCGC CACGTCCCGA CATATGGTGC TGAGCTCAGA ACAGCCCGAG GTGATCCTTT  
841 TAATGTGCTA GTCTACGTGC CCACTGGGTT TGCTGTGTTT GTGCCGACTG AGCGAGATT  
901 TCAGAGGAGG GATCTGGTCC GTTCCAGAC CTGCTGCTTC CGGCATCA

The Inverted Terminal Repeat (ITR) is shown in bold. Enzyme sites of interest are underlined with the enzyme name below. Putative TATA for E4 region is also shown.

Fig 4.

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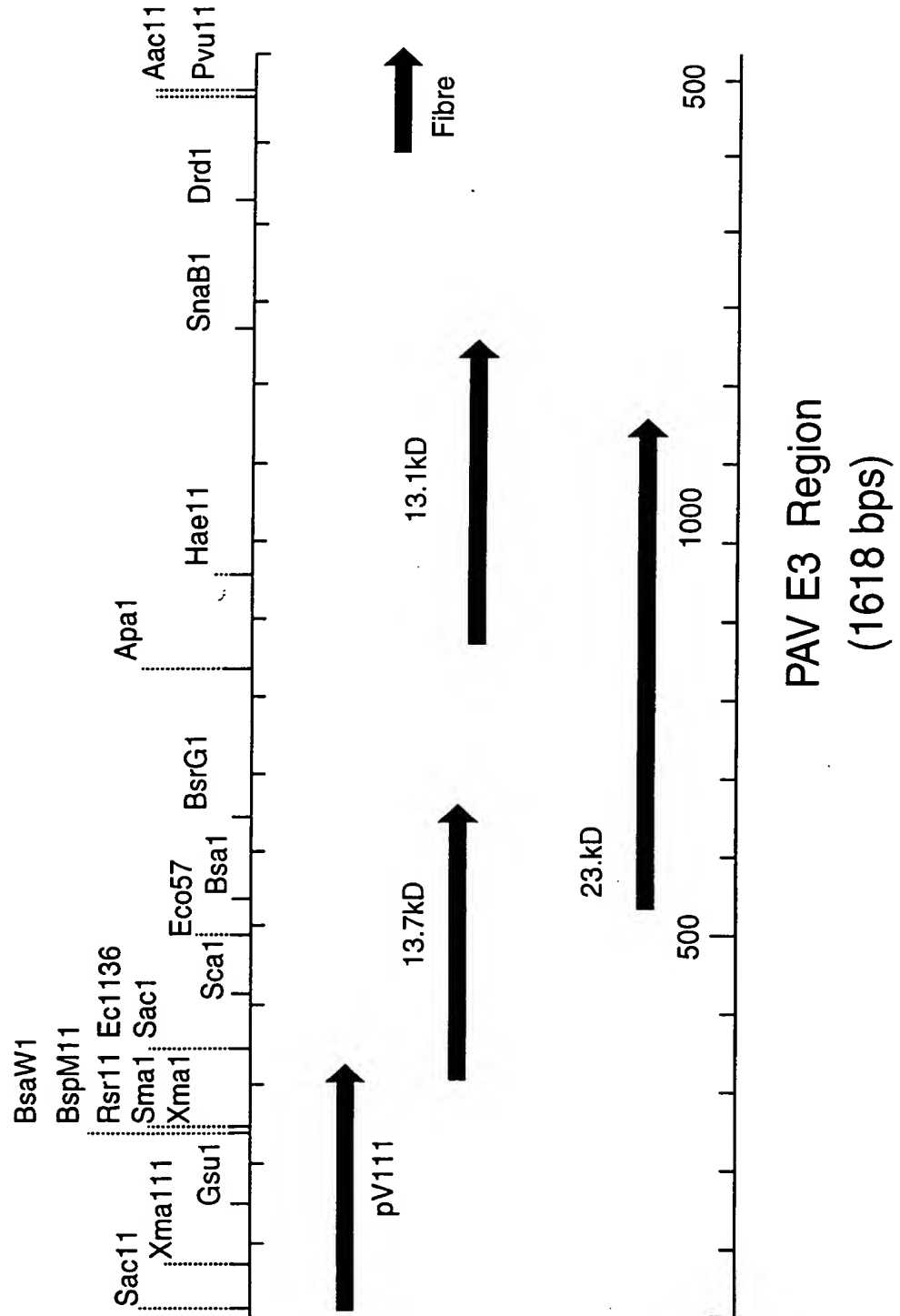
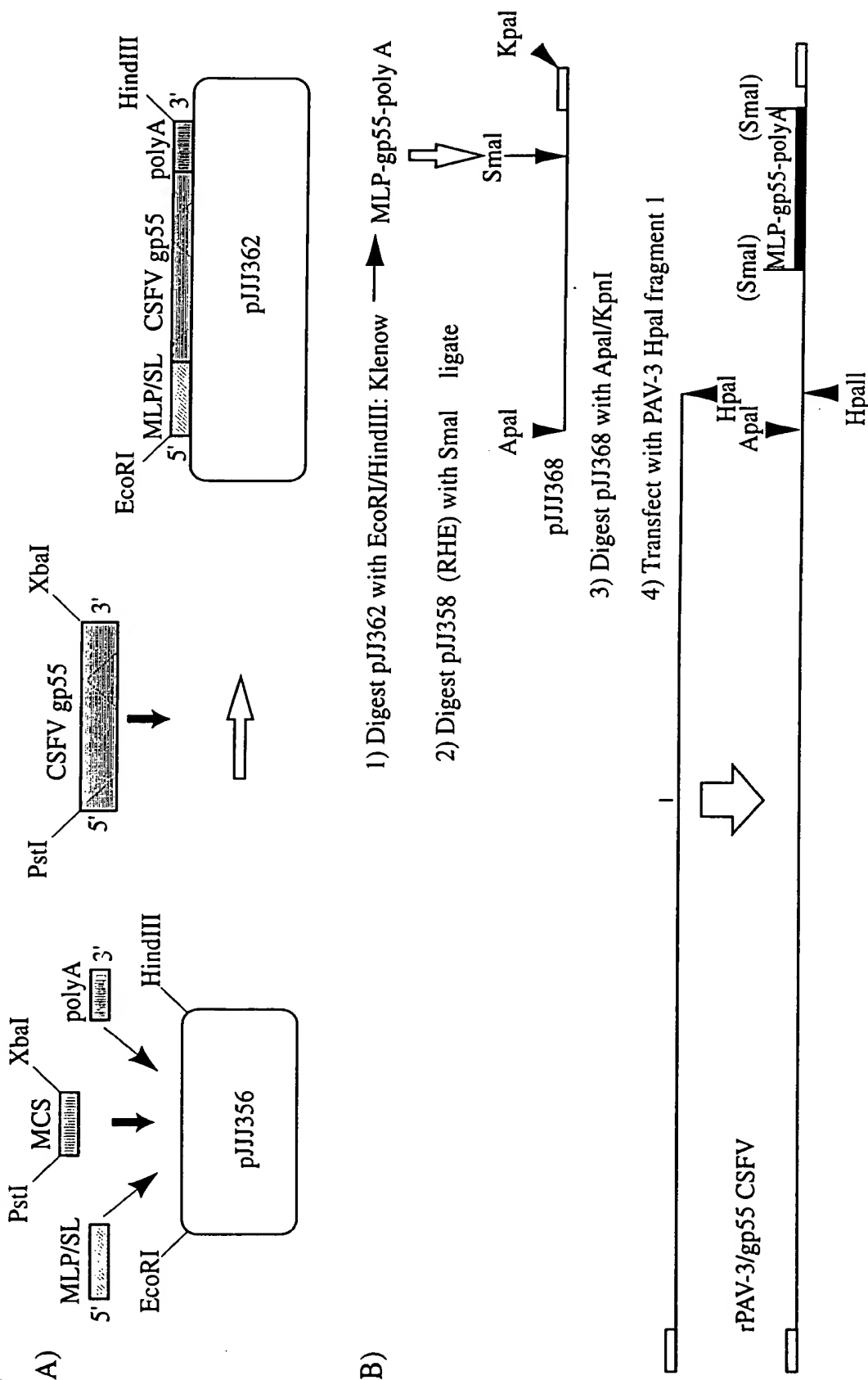


Fig 5.

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Fig 6.



APPROVED	C.G. FIG.	
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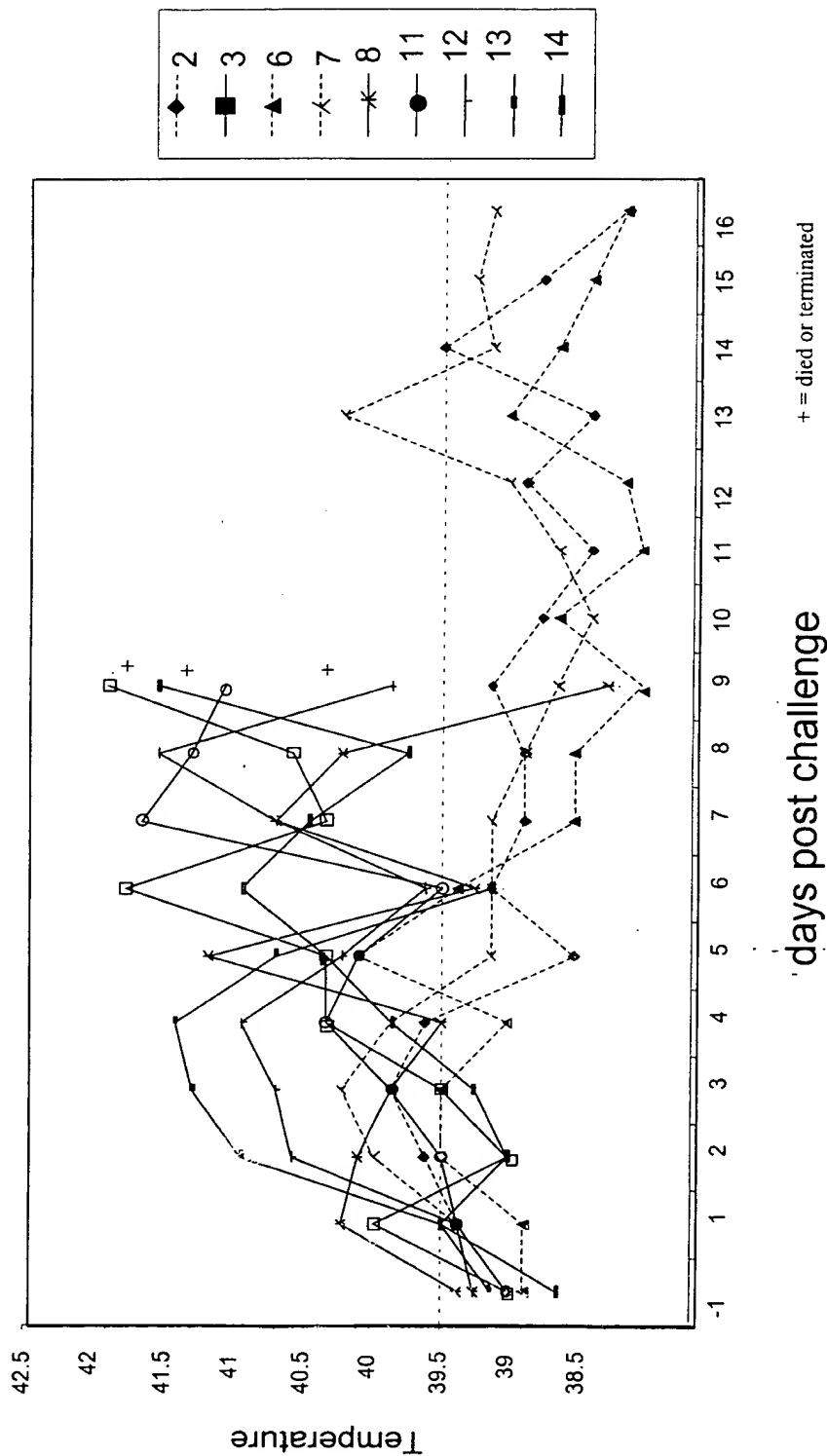


FIGURE 7

APPROVED	J.C. FIG.	
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FIGURE 8

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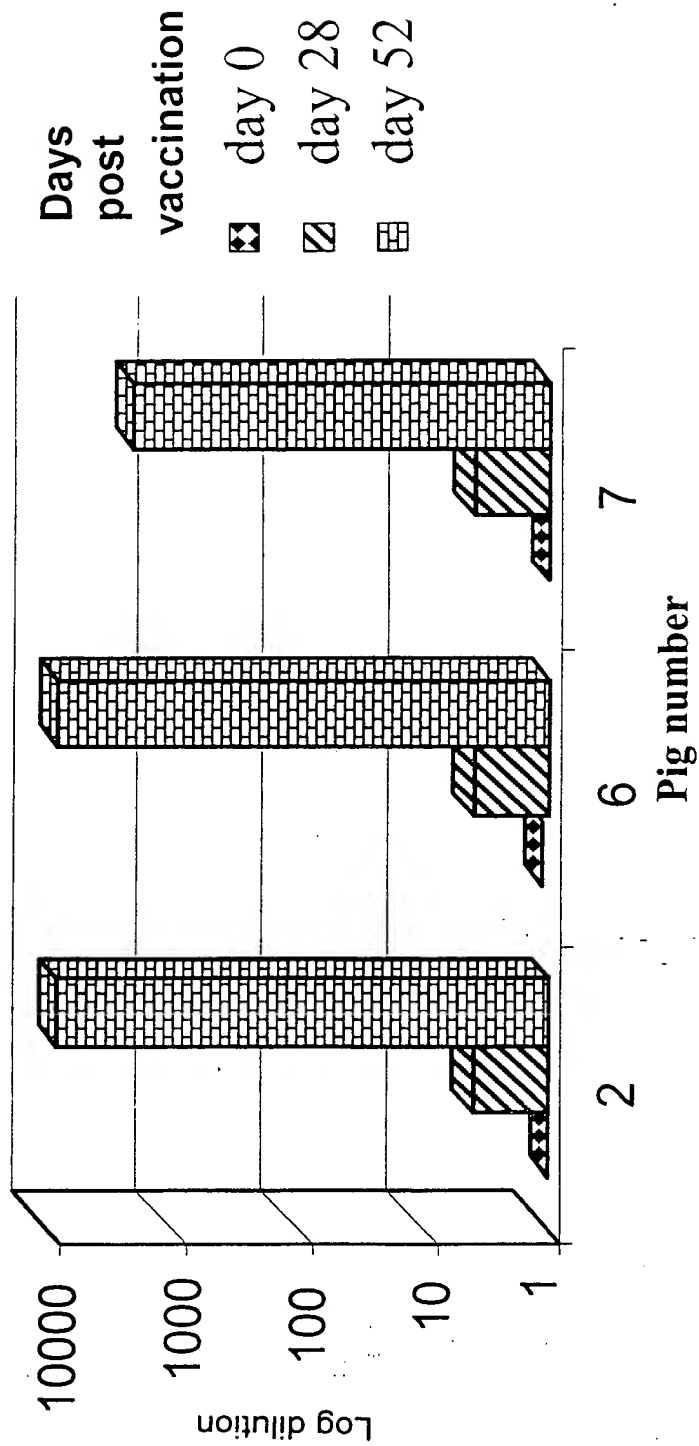
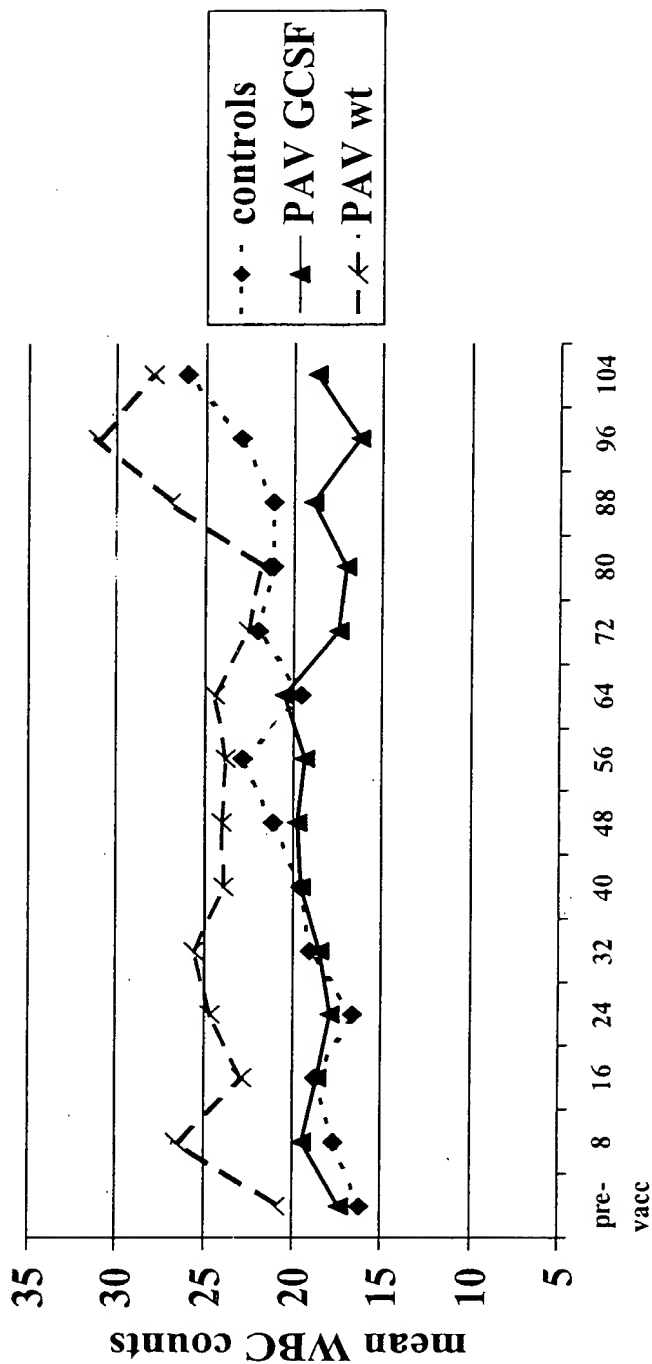


FIGURE 9



Hours post vaccination

FIGURE 10

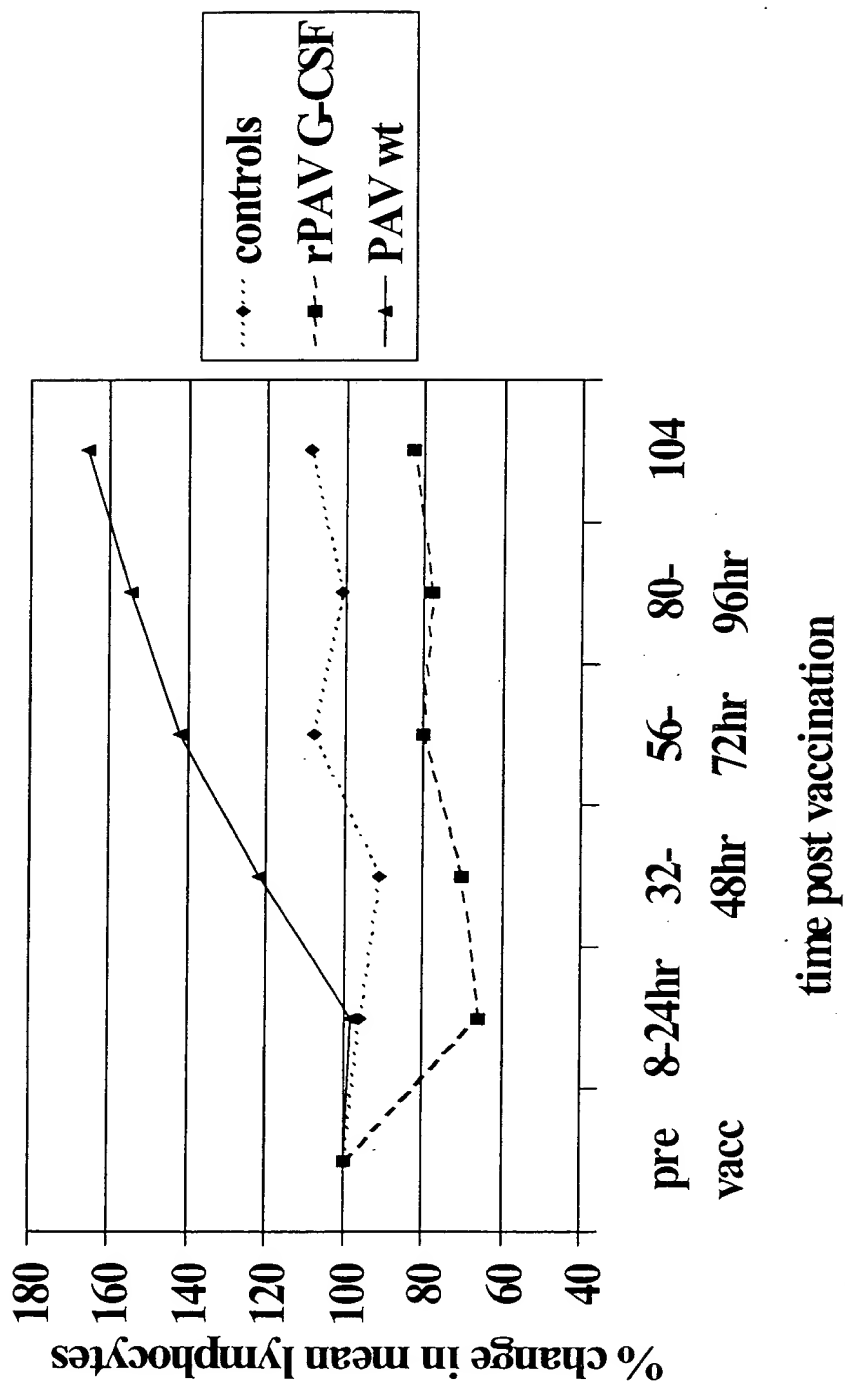


FIGURE 11

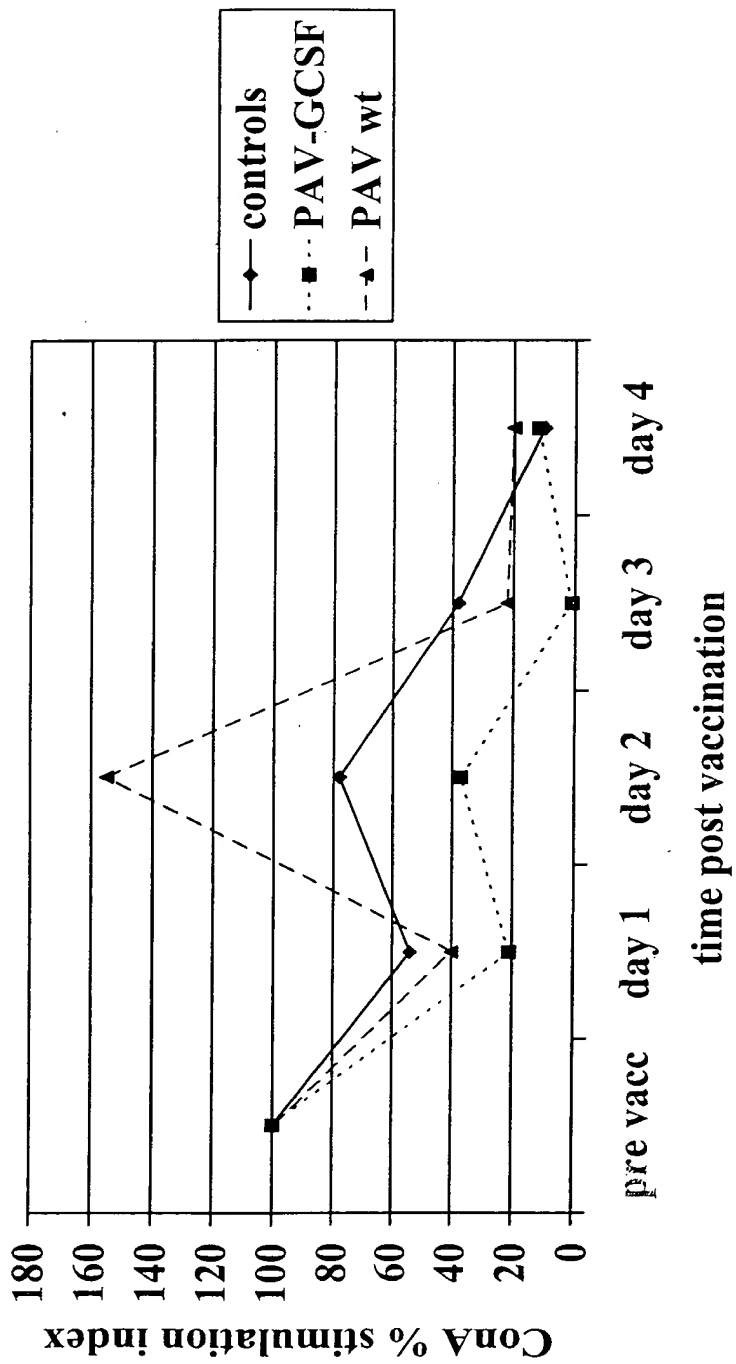
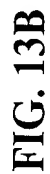
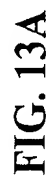


FIGURE 12



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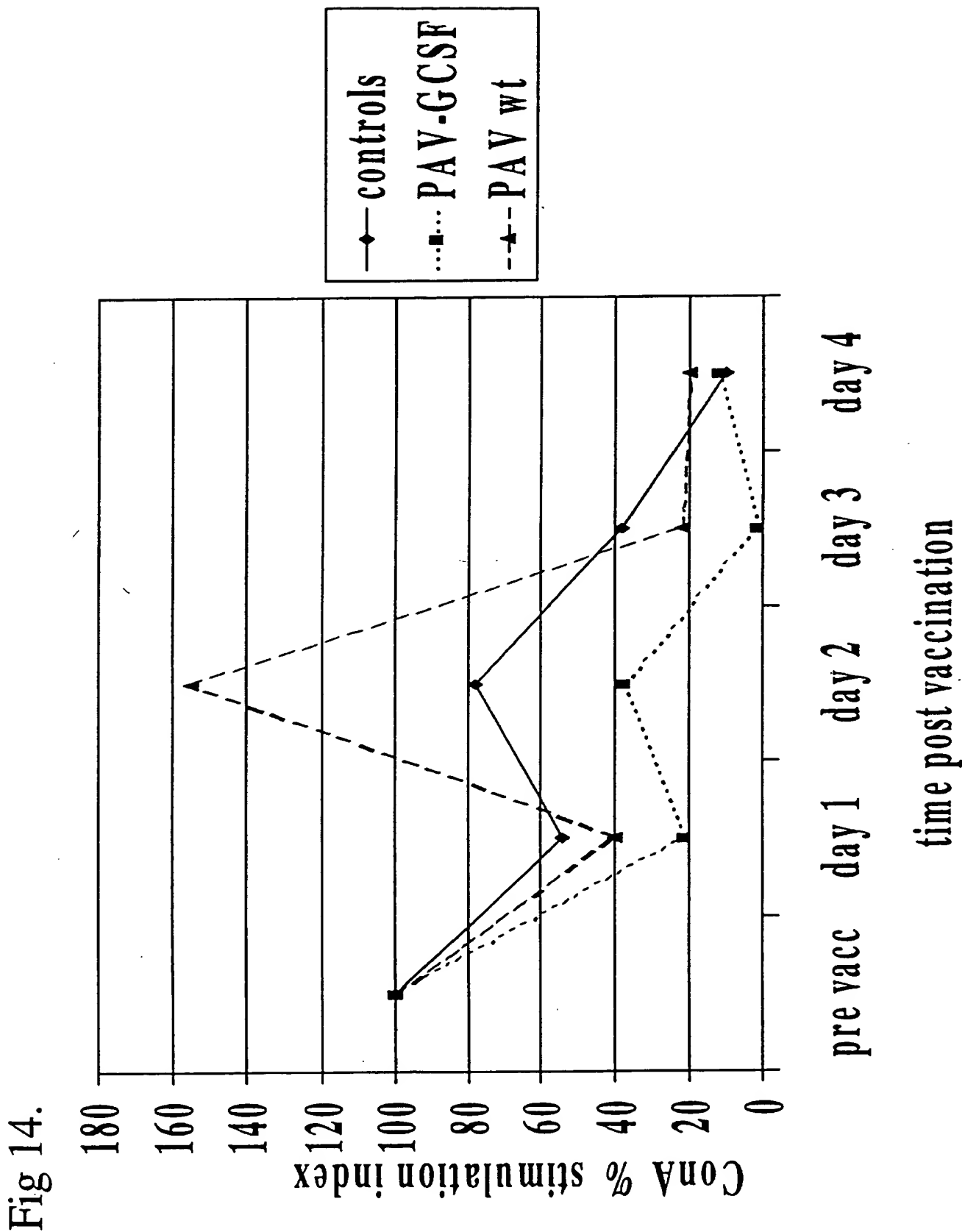


Fig 15.

